Claims

1. A method of analyzing a sequence of a polynucleotide of interest, comprising the steps of:

a) incorporating one member of a specific binding pair at the end of each strand of a double stranded polynucleotide of interest, the member being of the same type for both strands,

b) immobilizing both strands of the polynucleotide to a solid support provided with the other member of the specific binding pair,

c) annealing sequencing primers to the immobilized strands,

d) sequencing both strands by the chain termination method.

2. A method according to claim 1, characterized in that the polynucleotide of interest is amplified before or in connection with step a).

3. A method according to claim 2, characterized in that said polynucleotide is amplified by polymerase chain reaction extension of a first and second amplification primer, one primer being annealed to each strand of the double stranded polynucleotide, wherein both primers comprise the member of the specific binding pair, the member being of the same type for both primers, thereby producing copies of both strands of the polynucleotide bonded to said member of the specific binding pair.

4. A method according to any of the claims 1-3, characterized in that the immobilization in step b) is made under denaturating conditions.

5. A method according to any of the claims 1-3, characterized in that the strands are denatured after immobilization in step b).

6. A method according to claim 1, characterized in that the sequencing primers are differently labelled.

7. A method according to claim 6, characterized in that the labels are different fluorescent dyes.

8. A method according to claim 1, characterized in that the solid support is a manifold having a plurality of individual solid phase members.

9. A method according to claim 8, characterized in that the solid phase members are adapted for cooperation with a corresponding set of receptacles.

10. A metod according to claim 1, characterized in that the specific binding pair is selected from biotin - avidin, biotin - streptavidin, cystein - thiol groups, antigen - antibody, lectin - sugar.

11. A kit for use in analyzing the sequence of a polynucleotide of interest comprising:

(a) a solid support,

(b) amplification primers comprising one member of a specific binding pair, the member being of the same type for both primers,

(c) sequencing primers.

12. A kit according to claim 11, characterized in that the solid support is a manifold having a plurality of individual solid phase members and that the sequencing primers are differently labelled.

13. The method according to any of claims 1-10 for confirmatory sequencing e.g. DNA diagnosis, in forensic analysis, HLA typing.